RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/586, 374

Source: _____ TFWR

Date Processed by STIC: _____ 08/01/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/586,374_   CRF Edit Date: _08/01/2006_
                                 Edited by: _DH_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

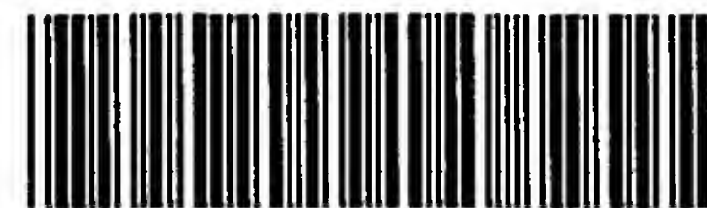____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

__✓_ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

IFWP

RAW SEQUENCE LISTING   DATE: 08/01/2006
PATENT APPLICATION: US/10/586,374   TIME: 15:52:40

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\07312006\J586374.raw**

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 4 <110> APPLICANT: Robert G.K. Donald
 5        Paul Liberator
 6        Xiaotian Zhong
 8 <120> TITLE OF INVENTION: Coccidian parasite casein kinase I as a
 9        chemotherapeutic target for antiprotozoal agents
12 <130> FILE REFERENCE: 21554P
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C--> 14 <140> **CURRENT APPLICATION NUMBER: US/10/586,374**
C--> 14 <141> **CURRENT FILING DATE: 2006-07-14**
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14 <150> PRIOR APPLICATION NUMBER: 60/537,094
15 <151> PRIOR FILING DATE: 2004-01-16
17 <150> PRIOR APPLICATION NUMBER: PCT/US2005/000955
18 <151> PRIOR FILING DATE: 2005-01-12
20 <160> NUMBER OF SEQ ID NOS: 45
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2182
26 <212> TYPE: DNA
27 <213> ORGANISM: Eimeria tenella
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (715)...(1722)
33 <400> SEQUENCE: 1
34 gcggccgcgt cgacgtcttt gctgccgcac agggagcagc agcagccgcc gacccgatcc 60
35 cttgggagcc caccaagtgc tgcgcttgct tagcagctac aggagctgcc gcggggttgc 120
36 tccctgaggc agcgtgcatg tatggtccgg cagccagctt ggtgtcgcag ccgtacttct 180
37 tggaagcgag agagactgtg ggagagcgca aatcactcca gccgcttcca ggggagtctg 240
38 gggaccgcag gagcgttgga ggctgcctgc cggcataaac aggaacaagc gcattcttat 300
39 tcttctgtgg ttgctgagtt ctggctgcgt tcaaggggt tcacctcttc cccttctggc 360
40 gagttttgc tgcgtctttc cctaagaagc agcgccacgt gcgtggcgtg cctcagcctg 420
41 acgcggtgca ccttttacgt aagagcgtcg atagcatcgg tcatctacag cagcgtgctg 480
42 ctgcttccgt gacctttaca ctgcttgtgg cgggccgtct tgtagagggg ccatctgctt 540
43 gttcgctgct ggacgcagac ccggcgcccg acatttccgg cagccgggca gttgagataa 600
44 accggctgcc cggtggccgt cgaaattgaa gcaggatctc tacagtaagg aacaaatcgc 660
45 gctattttta aggagtgtgt atacttgggg cgttactcgt gagtattgct gatg atg    717
46                                                            Met
47                                                             1
48 gac gtc cgt gtg ggg ggt aag tat cgt ttg ggg agg aag att ggg agc  765
49 Asp Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser
50          5                   10                  15
51 gga tcc ttc ggc gac atc tac ctt ggt acg aac atc tca aca gga gat  813
52 Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asn Ile Ser Thr Gly Asp
53          20                  25                  30
54 gaa gtc gct atc aaa ttg gaa agc gtg cgg tct agg cat cca caa cta  861
```

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 56 Glu Val Ala Ile Lys Leu Glu Ser Val Arg Ser Arg His Pro Gln Leu
 57      35                  40                  45
 58 atc tat gaa agc aag ctg tac aaa atc cta acg ggt gga atc gga atc    909
 59 Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly Ile
 60 50                  55                  60                  65
 61 ccg act ctt tac tgg tat ggg atc gag ggg gat tac aac gtt atg att    957
 62 Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Ile
 63                  70                  75                  80
 64 att gag ctt ttg ggc ccg tct ctt gag gac ctc ttc agc att tgc aac   1005
 65 Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn
 66                  85                  90                  95
 67 aga aag ctt tct ttg aag act gtt ctg atg ctc gcc gac caa atg cta   1053
 68 Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu
 69             100                 105                 110
 70 aat cgt att gag ttc gtc cac agc aga cat ttc atc cat cga gac atc   1101
 71 Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp Ile
 72     115                 120                 125
 73 aag cct gac aat ttt ttg atc ggt agg ggc aaa aag atg tcc att gtt   1149
 74 Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile Val
 75 130                 135                 140                 145
 76 ttt gct atc gac ttt ggc ctc gca aag aag tac aga gat ccc aga aca   1197
 77 Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg Thr
 78             150                 155                 160
 79 cag tcc cat att cct tat cga gaa ggg aag aac ctg aca ggt acc gcg   1245
 80 Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala
 81             165                 170                 175
 82 agg tac gcc tct gtg aac acc cac ttg gga ata gaa cag agc agg cgc   1293
 83 Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg
 84             180                 185                 190
 85 gat gat ctg gaa gcg ctc ggc tac gtc tta atg tac ttc aac aga ggt   1341
 86 Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly
 87     195                 200                 205
 88 tcc tta ccc tgg caa gga tta aag gcc act acg aag aaa gat aaa tat   1389
 89 Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr
 90 210                 215                 220                 225
 91 gac aag att atg gag aag aag atg tcc acc cct att gaa gtc ctt tgc   1437
 92 Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu Cys
 93             230                 235                 240
 94 aaa caa ttt cca ttt gag ttt atc aca tat ctg aac tat tgc cgg tct   1485
 95 Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser
 96             245                 250                 255
 97 ctg cga ttc gaa gat cgc ccg gac tat tcc tat ttg aga cgg ttg ttc   1533
 98 Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu Phe
 99             260                 265                 270
100 aag gat ctt ttc ttc cgt gag gga tac cag tat gac ttt ata ttc gat   1581
101 Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp
102     275                 280                 285
103 tgg aca ttt ctg cat gct gag aga gag cgc gag cgt caa aga cga tcg   1629
104 Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg Ser
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RAW SEQUENCE LISTING   DATE: 08/01/2006
PATENT APPLICATION: US/10/586,374   TIME: 15:52:40

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\07312006\J586374.raw

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105 290                  295                 300                 305
106 atg gtc aac caa ggc gca gaa tca ggg aac cag tgg aga cga gac gcg   1677
107 Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp Ala
108                 310                 315                 320
109 tcg ggc aga gat cca ctt gga cgg ttg cct cag tta gaa ccg taa      1722
111 Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro *
112                 325                 330                 335
114 tctctttacg ggcagattgc cgtacgggtc ttctgctcat tcagtggcag tgccaccgca 1782
115 gtgctatctg aggctgtggc ttcaggatgt ggtagccagt taccatggtc acttgccctc 1842
116 gctaggacag ccttcgcagg gaaatgtcac agtagcctgc attatgtggt gtgagaactg 1902
117 ctagcgcatt cctgtagttg cttttacgaa gcaggatacg cagcgtgcat cacgcggtgg 1962
118 ttcgagcgct cgctacgcat cacagggctg tgaggcaagt tagtatcttt ggggacgag  2022
119 ttgagagtgt cagaatcgat agtctcaggg catgcaggcg aaatggaggc tgcgccagta 2082
120 gtgccagccg gtggcgaagg cgtcaaattt actttttttg ttgctgggga tattgttaga 2142
121 gcaacaactt gggtctagat gctactgata aaaaaaaaa                        2182
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 335
125 <212> TYPE: PRT
126 <213> ORGANISM: Eimeria tenella
128 <400> SEQUENCE: 2
129 Met Asp Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly
130 1               5                   10                  15
131 Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Thr Asn Ile Ser Thr Gly
132                 20                  25                  30
133 Asp Glu Val Ala Ile Lys Leu Glu Ser Val Arg Ser Arg His Pro Gln
134             35                  40                  45
135 Leu Ile Tyr Glu Ser Lys Leu Tyr Lys Ile Leu Thr Gly Gly Ile Gly
136     50                  55                  60
137 Ile Pro Thr Leu Tyr Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met
138 65                  70                  75                  80
139 Ile Ile Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys
140                 85                  90                  95
141 Asn Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met
142             100                 105                 110
143 Leu Asn Arg Ile Glu Phe Val His Ser Arg His Phe Ile His Arg Asp
144             115                 120                 125
145 Ile Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Ile
146     130                 135                 140
147 Val Phe Ala Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Arg
148 145                 150                 155                 160
149 Thr Gln Ser His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr
150                 165                 170                 175
151 Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Ile Glu Gln Ser Arg
152                 180                 185                 190
153 Arg Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg
154             195                 200                 205
155 Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys
156     210                 215                 220
157 Tyr Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
```

```
158 225                    230                 235                 240
159 Cys Lys Gln Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg
160                 245                 250                 255
161 Ser Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ser Tyr Leu Arg Arg Leu
162             260                 265                 270
163 Phe Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe
164         275                 280                 285
166 Asp Trp Thr Phe Leu His Ala Glu Arg Glu Arg Glu Arg Gln Arg Arg
167     290                 295                 300
168 Ser Met Val Asn Gln Gly Ala Glu Ser Gly Asn Gln Trp Arg Arg Asp
169 305                 310                 315                 320
170 Ala Ser Gly Arg Asp Pro Leu Gly Arg Leu Pro Gln Leu Glu Pro
171             325                 330                 335
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 2076
176 <212> TYPE: DNA
177 <213> ORGANISM: Toxoplasma gondii
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (898)...(1872)
183 <400> SEQUENCE: 3
184 cctcgttttg cttcattccc cgccttttct ctgtagctaa ccaaaggaac aaagtcagcg 60
185 gtagaagccg tttcttctgt ccgcttccca ctcttcccgt tcggctgccc ctgcagagcg 120
186 ccctttctat gcgttgccac ccgtctgcaa gtatcgcgtc tttcgtctca tcagtgattt 180
187 tctttgcgtg tcgcgttcgg gacgcccttt tctctcctca actaactagc agacgtttct 240
188 tccgtcccgc atgcgacagc gaagggcacg tcccccccagt tcttcatcgc ccacctgttg 300
189 tgcaacttgt cgcccgtcgt tcttcacttc ttctctccca tcctctcgtg actcttcctc 360
190 tcgagaactc tttctgtcga actctcaacc cccacgactg ctggtttcgt ggccgtcccg 420
191 catgcacctt gtgtcccgcc gccttggcgc aaacacccgc tttctctgct gtccgcctcc 480
192 cggtggactt ctctccgtgt ttttcgtgt tgccaaaagt ttgtctgctt tgacgtttct 540
193 ctgctcaccc attgcccgct cttgatgagg aacgctccac attgacagcg aactcacagc 600
194 acgcaccctc cgcgagcgga ctttcacgag cgaggcaaga atccatcgtc accccgccta 660
195 cacgtacact actccacttg ggtgcccacg cgcggcttct gggagacaga gacggtcctc 720
196 gttttccgtg tcagaacttt gtcgaggaaa cgctgctgct ggcagcgggg attgtgaccc 780
197 ccctcggcga acgggcgaag ccgccctgtc gcgcgtcgcg actcagctga ggcgacaggc 840
198 ggtcggcggc gtgacctctc tttctttttg cattcggccc tgattgcagc acgaagg atg 900
199                                                             Met
200                                                             1
201 gag gtc agg gtc gga ggc aag tac cga ctt ggt cgg aag atc ggc agc  948
202 Glu Val Arg Val Gly Gly Lys Tyr Arg Leu Gly Arg Lys Ile Gly Ser
203             5                   10                  15
204 ggg tca ttc ggt gat att tat atc ggt gca aac att ttg acg ggg gat  996
205 Gly Ser Phe Gly Asp Ile Tyr Ile Gly Ala Asn Ile Leu Thr Gly Asp
206         20                  25                  30
207 gag gtg gcg atc aag ttg gag tct atc aag tcg aag cac ccg cag ctg  1044
208 Glu Val Ala Ile Lys Leu Glu Ser Ile Lys Ser Lys His Pro Gln Leu
209     35                  40                  45
210 ctc tat gag tcg aag ctg tac aaa ctg ctg gct ggc ggc att ggg att  1092
211 Leu Tyr Glu Ser Lys Leu Tyr Lys Leu Leu Ala Gly Gly Ile Gly Ile
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RAW SEQUENCE LISTING   DATE: 08/01/2006
PATENT APPLICATION: US/10/586,374   TIME: 15:52:40

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\07312006\J586374.raw

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212  50                   55                  60                       65
213 ccc atg gtc cac tgg tac ggc atc gaa gga gac tac aat gtt atg gtt    1140
214 Pro Met Val His Trp Tyr Gly Ile Glu Gly Asp Tyr Asn Val Met Val
215                   70                  75                  80
216 atc gac ctt ctc ggc cct tct ctg gag gac ctt ttc agt atc tgc aat    1188
217 Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Ser Ile Cys Asn
218              85                  90                  95
219 cgc aaa ctc tct ctc aag acg gtg ttg atg ctc gca gac cag atg ctc    1236
221 Arg Lys Leu Ser Leu Lys Thr Val Leu Met Leu Ala Asp Gln Met Leu
222          100                 105                 110
223 aac cgc atc gag ttt gtc cat agc aag aac ttc atc cat cgc gat atc    1284
224 Asn Arg Ile Glu Phe Val His Ser Lys Asn Phe Ile His Arg Asp Ile
225     115                 120                 125
226 aaa ccc gac aac ttc ctc att ggc cgt gga aag aag atg tcc gtc gtc    1332
227 Lys Pro Asp Asn Phe Leu Ile Gly Arg Gly Lys Lys Met Ser Val Val
228 130                 135                 140                 145
229 tac atc atc gat ttc ggt ttg gca aag aaa tat cga gac cca aag act    1380
230 Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Pro Lys Thr
231              150                 155                 160
232 cag caa cat atc cca tac agg gaa ggc aag aac cta aca ggc aca gcg    1428
233 Gln Gln His Ile Pro Tyr Arg Glu Gly Lys Asn Leu Thr Gly Thr Ala
234              165                 170                 175
235 cgt tac gct tcc atc aac acc cac ctg ggg atc gag cag agt cgg cga    1476
236 Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg Arg
237          180                 185                 190
238 gac gac cta gag gcg ctc ggt tac gtt ctc atg tac ttc aat aga ggt    1524
239 Asp Asp Leu Glu Ala Leu Gly Tyr Val Leu Met Tyr Phe Asn Arg Gly
240     195                 200                 205
241 tct ctt ccg tkg cag ggt ctg aag gcg acg acg aag aag gac aaa tac    1572
```
W--> **242 Ser Leu Pro Xaa Gln Gly Leu Lys Ala Thr Thr Lys Lys Asp Lys Tyr**
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243 210                 215                 220                 225
244 gac aag att atg gag aag aaa atg tct act ccc atc gaa att ttg tgc    1620
245 Asp Lys Ile Met Glu Lys Lys Met Ser Thr Pro Ile Glu Ile Leu Cys
246              230                 235                 240
247 aag cat ttc cca ttc gag ttc atc acc tac ttg aat tac tgc cgg tcc    1668
248 Lys His Phe Pro Phe Glu Phe Ile Thr Tyr Leu Asn Tyr Cys Arg Ser
249          245                 250                 255
250 ctg cgc ttc gag gat cgt cct gac tac gca tac ttg cga cgc ctg ttc    1716
251 Leu Arg Phe Glu Asp Arg Pro Asp Tyr Ala Tyr Leu Arg Arg Leu Phe
252          260                 265                 270
253 aaa gac ttg ttt ttt aga gag gga tat cag tac gac ttc atc ttc gac    1764
254 Lys Asp Leu Phe Phe Arg Glu Gly Tyr Gln Tyr Asp Phe Ile Phe Asp
255     275                 280                 285
256 tgg act ttc atc aac acg gag aag gat cgc gcg agt cga aga agc cag    1812
257 Trp Thr Phe Ile Asn Thr Glu Lys Asp Arg Ala Ser Arg Arg Ser Gln
258 290                 295                 300                 305
259 caa gtt tat gtg gaa gac aac cgg caa gtt gag gag aat cag aac gag    1860
260 Gln Val Tyr Val Glu Asp Asn Arg Gln Val Glu Glu Asn Gln Asn Glu
261              310                 315                 320
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VERIFICATION SUMMARY   DATE: 08/01/2006
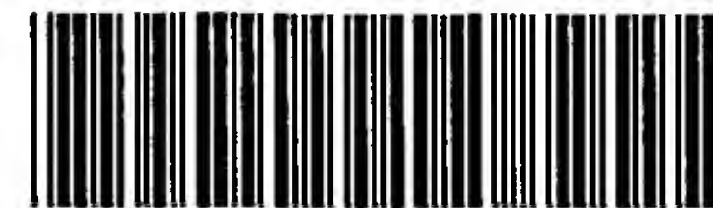PATENT APPLICATION: **US/10/586,374**   TIME: 15:52:41

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\07312006\J586374.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:242 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:3
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1572
L:1061 M:283 W: Missing Blank Line separator, <220> field identifier

Raw Sequence Listing before editing
(for reference only)

IFWP

RAW SEQUENCE LISTING   DATE: 07/26/2006
PATENT APPLICATION: **US/10/586,374**   TIME: 15:08:44

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\07262006\J586374.raw**

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      4 <110> APPLICANT: Robert G.K. Donald
      5        Paul Liberator
      6        Xiaotian Zhong
      8 <120> TITLE OF INVENTION: Coccidian parasite casein kinase I as a
      9        chemotherapeutic target for antiprotozoal agents
     12 <130> FILE REFERENCE: 21554P
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/586,374
C--> 14 <141> CURRENT FILING DATE: 2006-07-14
     14 <150> PRIOR APPLICATION NUMBER: 60/537,094
     15 <151> PRIOR FILING DATE: 2004-01-16
     17 <150> PRIOR APPLICATION NUMBER: PCT/US2005/000955
     18 <151> PRIOR FILING DATE: 2005-01-12
     20 <160> NUMBER OF SEQ ID NOS: 45
     22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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Does Not Comply
Corrected Diskette Needed

(P9-1)

ERRORED SEQUENCES

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   1057 <210> SEQ ID NO: 45
   1058 <211> LENGTH: 29
   1059 <212> TYPE: DNA
   1060 <213> ORGANISM: Artificial Sequence
W--> 1061 <220> FEATURE:
   1062 <223> OTHER INFORMATION: oligonucleotide
   1064 <400> SEQUENCE: 45
   1065 gtttccgcag agcttcaaga gcatctgtt                    29
E--> 1070 - 1 -
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deleted

VERIFICATION SUMMARY   DATE: 07/26/2006
PATENT APPLICATION: **US/10/586,374**   TIME: 15:08:45

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\07262006\J586374.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:242 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:3
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1572
L:1061 M:283 W: Missing Blank Line separator, <220> field identifier
L:1070 M:254 E: No. of Bases conflict, this line has no nucleotides.